## Amendments to the Specification

**Please replace the paragraph beginning at page 23, line 4 with the following replacement paragraph:**

Cellular mRNA was isolated using the ~~Micro Fast Track~~™ MICRO FAST TRACK™ kit (Invitrogen, Karlsruhe, Germany) and cDNA synthesized using the ~~cDNA Cycle~~™ cDNA-CYCLE™ kit (Invitrogen, Karlsruhe, Germany). PCR was performed in a master mix containing 1 x PCR buffer (PE/Applied Biosystems, Forster City, CA), 2 mM of each desoxyribonucleotide triphoshate (Stratagene, LaJolla, CA), 2 µM of uPAR-specific primers for uPAR-exons 1 and 6 (SEQ ID No. 17: forward: CTCCACACCTGCGTCCCA, SEQ ID No. 18: reverse: CTTGCAGCTGTAACACTG; Metabion, Martinsried, Germany) (Fig. 16), 1.0 U ~~AmpliTaq GoldTM~~ AMPLITAQ GOLD™ DNA polymerase (PE/Applied Biosystems), and 2 µl cDNA in a total volume of 50 µl. The amplification profile consisted of denaturation at 94 °C for 1 min, annealing at 49 °C for 45 sec, and primer extension at 72 °C for 45 sec in a 30-cycle reaction. Twenty µl of the PCR products were separated electrophoretically in 4-12 % TBE-PAGE (Novex), stained with SYBR Green (Biozym Diagnostica GmbH, Hess. Oldendorf, Germany), and analyzed with the Fluor-S MultiImager (BioRad, München, Germany) using the Multi-Analyst PC software (BioRad, München, Germany). As an internal control, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was co-amplified. Amplified cDNA was separated by agarose gel electrophoresis (2%) and visible PCR products were sequenced.

**Please replace the paragraph beginning at page 23, line 26 with the following replacement paragraph:**

Based on the ~~LightCycler~~ LIGHTCYCLER technology (Roche, Mannheim, Germany), real-time RT-PCR assays were established in order to quantify expression of uPAR mRNA variants and of the reference gene GAPDH. Specific PCR products were quantified by the detection of fluorescence signals of site-specific hybridization probes (assays for uPAR mRNA variants) or of the intercalating dye SYBR Green (assay for GAPDH mRNA).

**Please replace the paragraph beginning at page 28, line 16 with the following replacement paragraph:**

For quantification of del2+3+4 mRNA (encompassing exons 2, 3, and 4) and del4+5 mRNA (encompassing exons 2, 3, and 6 and lacking exons 4 and 5, respectively) two highly sensitive real-time RT-PCR assays applying the ~~LightCycler~~ LIGHTCYCLER technology were established. The concentration of standard DNA for capillary coating in this system was exactly determined by HPLC calibration. This clearly improved the sensitivity and the reproducibility of the assay (CV<10 %; Fig. 19).

**Please replace the paragraph beginning at page 31, line 11 with the following replacement paragraph:**

The presence of more than one mRNA form derived from the same gene is a common observation for a growing number of proteins. These forms may result from alternative splicing, retained intronic segments or the utilization of alternative transcription initiation or polyadenylation sites. Variation of the splicing process occurs during tumor progression and may play a major role in tumorigenesis. Especially for many cancer-associated genes - such as CD44, WT-1, survivin, mdm2, MUC-1, and VEGF - a broad spectrum of alternatively and/or aberrantly splice variants with different and often oncogenic functions have been identified. However, only a few of the described mRNA splice variants are both expressed in a biological relevant concentration and detectable in a significant amount. Furthermore, often it is unknown whether these variant transcripts are translated into protein. Characterization of splice variants of a gene may still be of importance. In addition to any biological role, such variants may have the potential of being useful diagnostic markers. For quantification of uPAR mRNA variants encompassing exons 2 to 4 (del2+3+4) and encompassing exons 2, 3, and 6 (del4+5), respectively, two highly sensitive real-time RT-PCR assays based on ~~LightCycler~~ LIGHTCYCLER technology were established. Analysis of its expression in breast cancer tissues as shown in the present study, or in other cancer tissues (unpublished observation), indicates that the mRNA variant del4+5 is expressed frequently and independently of uPAR variants covering exon 4 (*i.e.* uPAR-wt and del5). In about 25 % of the analyzed breast carcinomas, the mRNA expression ratio of del4+5 in relation to del2+3+4 was greater than 0.5 indicating that the del4+5 mRNA splice variant could be of physiological significance. In addition, it was demonstrated - in this small but representative set of breast cancer specimens - that high del4+5 mRNA levels are significantly associated with a short disease-free survival of the patients, whereas uPAR antigen and del2+3+4 mRNA did not. It is tempting to speculate that the weak prognostic impact of uPAR antigen content of tumor tissue extracts or cytosols in comparison to the impact of other components of the plasminogen system such as uPA and PAI-1 is due to a masking of the levels of prognostic relevant uPAR variants by other uPAR forms. The preliminary observation that del4+5 protein expressed in CHO cells does not interact with uPA raises the questions, if there are any other interaction partners and if there is an uPA-independent tumorbiological role of this cell surface-associated receptor variant lacking DII.